

5' AAA CCT TCA CCT CTC ATG CTG AAG CTC ACA CCC TTG CCC TCC AAG ATG AAG GTT
M L K L T P L P S K M K V

TCT GCA GCG CTT CTG TGC CTG CTG CTC ATG GCA GCC ACT TTC AGC CCT CAG GGA
S A A L L C L L L M A A T F S P Q G

CTT GCT CAG CCA GAT TCA GTT TCC ATT CCA ATC ACC TGC TGC TTT AAC GTG ATC
L A Q P D S V S I P I T C C F N V I

AAT AGG AAA ATT CCT ATC CAG AGG CTG GAG AGC TAC ACA AGA ATC ACC AAC ATC
N R K I P I Q R L E S Y T R I T N I

CAA TGT CCC AAG GAA GCT GTG ATC TTC AAG ACC AAA CGG GGC AAG GAG GTC TGT
Q C P K E A V I F K T K R G K E V C

GCT GAC CCC AAG GAG AGA TGG GTC AGG GAT TCC ATG AAG CAT CTG GAC CAA ATA
A D P K E R W V R D S M K H L D Q I

TTT CAA AAT CTG AAG CCA TGA GCC TTC ATA CAT GGA CTG AGA GTC AGA GCT TGA
F Q N L K P

AGA AAA GCT TAT TTA TTT TCC CCA ACC TCC CCC AGG TGC AGT GTG ACA TTA TTT

TAT TAT AAC ATC CAC AAA GAG ATT ATT TTT AAA TAA TTT AAA GCA TAA TAT TTC

FIGURE 1A

TTA AAA AGT ATT TAA TTA TAT TTA AGT TGT TGA TGT TTT AAC TCT ATC TGT CAT
495 504 513 522 531 540

ACA TCC TAG TGA ATG TAA AAT GCA AAA TCC TGG TGA TGT GTT TTT TGT TTT TGT
549 558 567 576 585 594

TTT CCT GTG AGC TCA ACT AAG TTC ACG GCC AAA NGT CAT TGT TCT CCC TCC TAC
603 612 621 630 639 648

CNG TNC GTA GTG TTG TGG GGT CCT CCC NTG GAT CAT CAA GGT GAA ACA CTT AGG
657 666 675 684 693 702

TAT TCT TTG GCA ATC AGT GCT CCT GTA AGT CAA ATG TGT GCT TTG TAC TGC TGT
711 720 729 738 747 756

TGT TGA AAT TGA NGT TAC TGT ANA TAA CTA TGG AAT TTT GAA AAA AAA TTT CAA
765 774 783 792 801 810

AAA GAA AAA NAT ATA TAT AAT TTA AAA CTA AAA AAA AAA AAA AAA A 3'
819 828 837 846 855

FIGURE 1B

1	M	L	K	L	T	P	L	P	S	K	M	K	V	S	A	A	L	L	C	L	L	L	M	A	A	T	F	S	P	Q	965517	
1	M	W	K	P	M	P	S	P	S	N	M	K	A	S	A	A	L	L	C	L	L	L	T	A	A	A	F	S	P	Q	GI 288397	
1	M	-	-	-	-	-	-	-	-	-	-	-	K	V	S	A	A	L	L	C	L	L	L	I	A	A	T	F	I	P	Q	GI 338809
31	G	L	A	Q	P	D	S	V	S	I	P	I	T	C	C	F	N	V	I	N	R	K	I	P	I	Q	R	L	E	S	965517	
31	G	L	A	Q	P	V	G	I	N	T	S	T	T	C	C	Y	R	F	I	N	K	K	I	P	K	Q	R	L	E	S	GI 288397	
21	G	L	A	Q	P	D	A	I	N	A	P	V	T	C	C	Y	N	F	T	N	R	K	I	S	V	Q	R	L	A	S	GI 338809	
61	Y	T	R	I	T	N	I	Q	C	P	K	E	A	V	I	F	K	T	K	R	G	K	E	V	C	A	D	P	K	E	965517	
61	Y	R	R	T	T	S	S	H	C	P	R	E	A	V	I	F	K	T	K	L	D	K	E	I	C	A	D	P	T	Q	GI 288397	
51	Y	R	R	I	T	S	S	K	C	P	K	E	A	V	I	F	K	T	I	V	A	K	E	I	C	A	D	P	K	Q	GI 338809	
91	R	W	V	R	D	S	M	K	H	L	D	Q	I	F	Q	N	L	K	P	965517												
91	K	W	V	Q	D	F	M	K	H	L	D	K	K	T	Q	T	P	K	L	GI 288397												
81	K	W	V	Q	D	S	M	D	H	L	D	K	Q	T	Q	T	P	K	T	GI 338809												

FIGURE 2

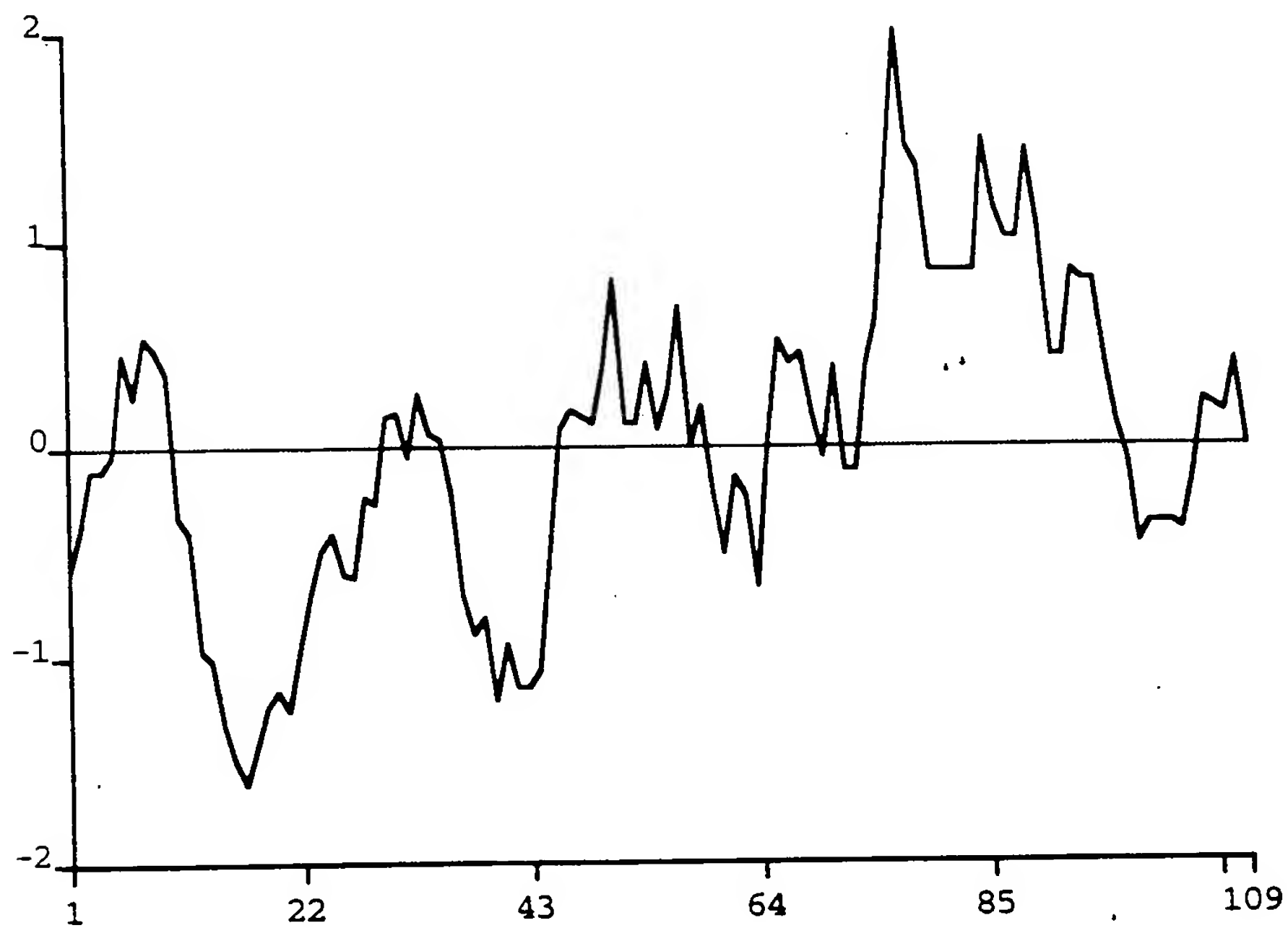


FIGURE 3

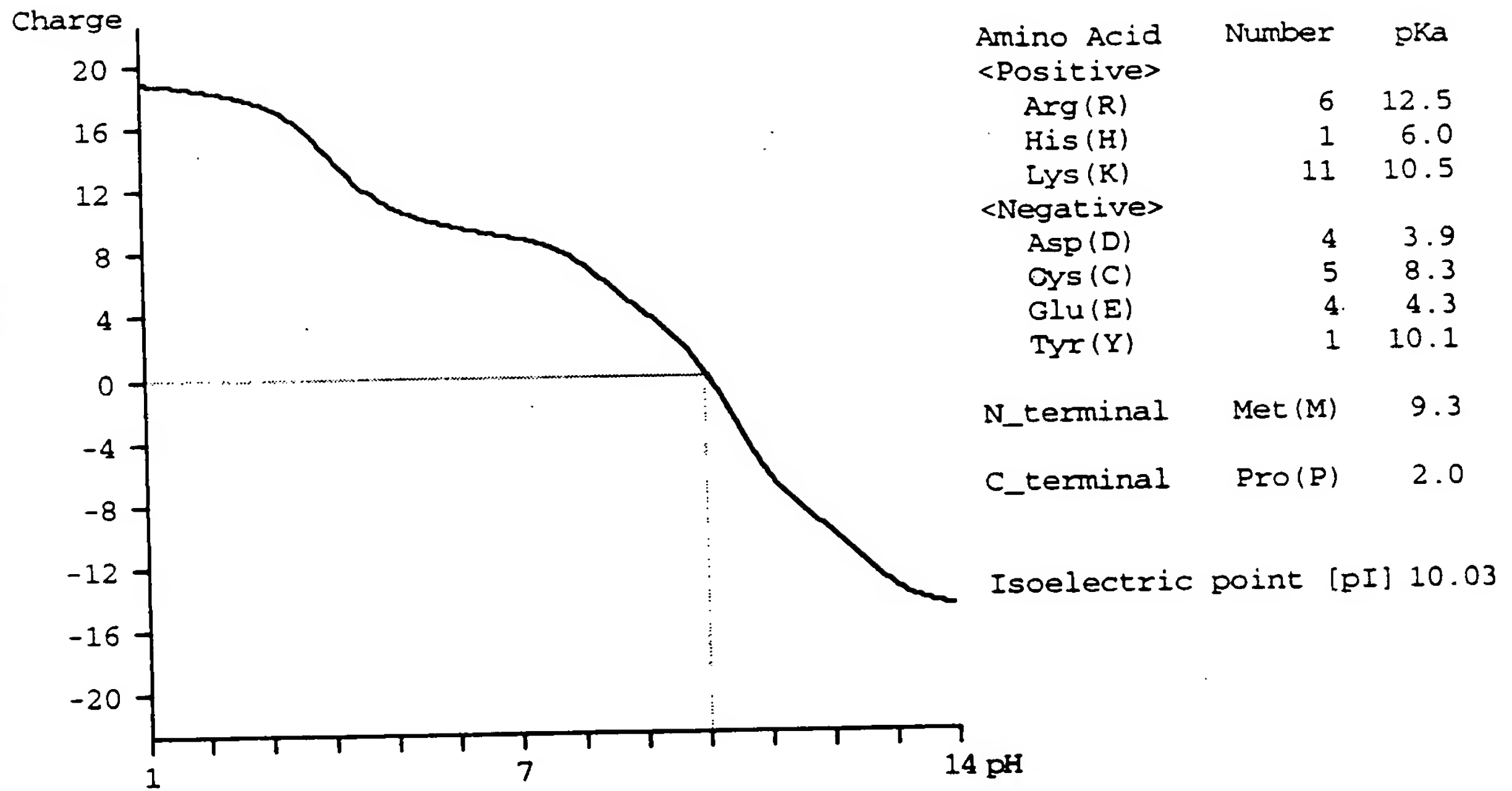


FIGURE 4

The Electronic Northern for Clone: 965517
and Stringency = 50

Library	Lib Description	Abun	Pct	Abur
PANCDIT03	pancreas, NIDDM, 57 M	1		0.145
MMLR1DT01	macrophages (adher PBMNC), M/F, 24-hr MLR	4		0.094
MMLR3DT01	macrophages (adher PBMNC), M/F, 72-hr MLR	2		0.066
MPHGLPT02	macrophages (adher PBMNC), M/F, treated LPS	1		0.045
TMLR3DT01	lymphocytes (non-adher PBMNC), M, 96-hr MLR	2		0.045
BLADTUT02	bladder tumor, carcinoma, 80 F	1		0.030
SYNORAT05	synovium, knee, rheumatoid, 62 F	1		0.026
LUNGNOM01	lung, 72 M, WM	1		0.026
MPHGNOT03	macrophages (adher PBMNC), M/F	2		0.025
BRSTNOT05	breast, 58 F, match to BRSTTUT03	1		0.015

FIGURE 5